

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:56:13 ; Search time 6 Seconds  
(without alignments)  
38.191 Million cell updates/sec

Title: US-09-362-286A-1

Perfect score: 136  
Sequence: 1 LAYNSNVNPIIYAFLENFRRYKQV 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US08 NEW PUB.pap:\*
- 2: /cgn2\_6/prodata/1/pubpaa/US06 NEW PUB.pap:\*
- 3: /cgn2\_6/prodata/1/pubpaa/US07 NEW PUB.pap:\*
- 4: /cgn2\_6/prodata/1/pubpaa/PCT NEW PUB.pap:\*
- 5: /cgn2\_6/prodata/1/pubpaa/US09 NEW PUB.pap:\*
- 6: /cgn2\_6/prodata/1/pubpaa/US10 NEW PUB.pap:\*
- 7: /cgn2\_6/prodata/1/pubpaa/US11 NEW PUB.pap:\*
- 8: /cgn2\_6/prodata/1/pubpaa/US60 NEW PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	92	67.6	420	6	US-10-992-577-6
2	92	67.6	522	6	US-10-510-018-2
3	89	65.4	114	6	US-10-995-561-836
4	89	65.4	388	6	US-10-995-561-838
5	89	65.4	389	6	US-10-995-561-837
6	87	64.0	417	6	US-10-992-577-44
7	86	63.2	400	7	US-11-127-877-55
8	81	59.6	216	6	US-10-980-388-99
9	81	59.6	340	7	US-10-980-388-117
10	81	59.6	340	7	US-11-127-877-53
11	81	59.6	430	6	US-10-992-577-8
12	80	58.8	559	6	US-10-521-162-4
13	80	58.8	712	6	US-10-521-162-12
14	77	56.6	92	6	US-10-521-162-34
15	77	56.6	480	6	US-10-521-162-40
16	76	55.9	355	7	US-11-068-686-4
17	76	55.9	355	7	US-11-127-877-64
18	76	55.9	432	6	US-10-992-577-2
19	75	55.1	532	7	US-11-127-877-42
20	74	54.4	350	7	US-11-165-024-3
21	73	53.7	391	7	US-11-127-877-52
22	72	52.9	358	6	US-10-055-877-176
23	70	51.5	358	6	US-10-055-877-177
24	70	51.5	429	7	US-11-127-877-51
25	70	51.5	466	7	US-11-127-877-50

Sequence 183, App  
Sequence 54, Appl  
Sequence 178, App  
Sequence 10, Appl  
Sequence 36, Appl  
Sequence 2, Appl  
Sequence 175, App  
Sequence 2, Appl  
Sequence 712, App  
Sequence 716, App  
Sequence 2, Appl  
Sequence 65, Appl  
Sequence 713, App  
Sequence 714, App  
Sequence 715, App  
Sequence 636, App  
Sequence 637, App  
Sequence 41, Appl  
Sequence 38, Appl  
Sequence 118, App

26 69 50.7 590 7 US-11-124-368A-183  
27 69 50.7 590 7 US-11-127-877-54  
28 68 50.0 333 6 US-10-055-877-178  
29 68 50.0 353 6 US-10-875-716-10  
30 67 48.3 360 6 US-10-959-310-36  
31 66 48.5 337 6 US-10-875-716-2  
32 66 48.5 338 6 US-10-055-877-175  
33 66 48.5 346 7 US-11-157-930-2  
34 66 48.5 359 6 US-10-995-561-712  
35 66 48.5 359 6 US-10-995-561-716  
36 66 48.5 359 6 US-10-876-787-2  
37 66 48.5 359 7 US-11-127-877-65  
38 66 48.5 388 6 US-10-995-561-713  
39 66 48.5 394 6 US-10-995-561-714  
40 66 48.5 394 6 US-10-995-561-715  
41 65 47.8 355 6 US-10-995-561-636  
42 65 47.8 362 6 US-10-995-561-637  
43 65 47.8 466 7 US-11-127-877-41  
44 64 47.1 318 7 US-11-127-877-38  
45 64 47.1 342 6 US-10-980-388-118

## ALIGNMENTS

RESULT 1  
US-10-992-577-6  
; Sequence 6, Application US/10992577  
; Publication No. US20050260687A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerald, Christophe P.G.  
; APPLICANT: Jones, Kenneth A.  
; APPLICANT: Bonini, James A.  
; APPLICANT: Borowsky, Beth E.  
; APPLICANT: Craig, Douglas A.  
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors  
; FILE REFERENCE: 57155-D/JEW  
; CURRENT APPLICATION NUMBER: US/10/992,577  
; CURRENT FILING DATE: 2004-11-18  
; PRIOR APPLICATION NUMBER: US/09/538,036  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/405,558  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 09/255,368  
; PRIOR FILING DATE: 1999-02-22  
; PRIOR APPLICATION NUMBER: 09/161,113  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-992-577-6

Query Match 67.6%; Score 92; DB 6; Length 420;  
Best Local Similarity 61.5%; Pred.No. 6.3e-07;  
Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAYNSNVNPIIYAFLENFRRYKQ 26  
DB 321 LAFGNSSVNPILYGFNFENFRGPG 346

RESULT 2  
US-10-510-018-2  
; Sequence 2, Application US/10510018  
; Publication No. US20050244896A1  
; GENERAL INFORMATION:  
; APPLICANT: Golz, Stefan  
; APPLICANT: Bruggemeier, Ulf  
; APPLICANT: Weingarten, Bernhard

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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:55:18 ; Search time 95.3333 Seconds  
(without alignments)  
118.336 Million cell updates/sec

Title: US-09-362-286a-1  
Perfect score: 136  
Sequence: 1 LAYNSGVSVPPIIYAFLSNFRKRYKQV 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.psp:\*  
2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.psp:\*  
3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.psp:\*  
4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.psp:\*  
5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.psp:\*  
6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.psp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	27	3	US-09-362-286-1
2	130	95.6	27	3	US-09-362-286-5
3	130	95.6	293	4	US-10-087-192-1464
4	130	95.6	339	4	US-10-087-192-1467
5	130	95.6	345	4	US-10-262-313-11
6	130	95.6	345	4	US-10-254-905-10
7	130	95.6	345	4	US-10-359-285-5
8	130	95.6	345	4	US-10-768-878-11
9	130	95.6	346	2	US-08-899-112-32
10	130	95.6	346	3	US-09-966-782A-10
11	130	95.6	346	3	US-09-992-331-11
12	130	95.6	346	3	US-09-825-751A-83
13	130	95.6	346	3	US-09-771-287-5
14	130	95.6	346	4	US-10-212-980-6
15	130	95.6	346	4	US-10-007-132-5
16	130	95.6	346	4	US-10-006-343-5
17	130	95.6	346	4	US-10-298-992-7
18	130	95.6	346	4	US-10-285-019-30
19	130	95.6	346	4	US-10-466-205-1
20	130	95.6	346	4	US-10-240-801A-11
21	130	95.6	346	5	US-10-851-438-83
22	130	95.6	347	4	US-10-262-313-10
23	130	95.6	347	4	US-10-254-905-9
24	130	95.6	347	4	US-10-768-878-10
25	130	95.6	348	3	US-09-966-782A-9
26	130	95.6	348	3	US-09-992-331-10
27	130	95.6	348	4	US-10-090-569-2

28	130	95.6	348	4	US-10-212-980-5	Sequence 5, Appli
29	130	95.6	348	4	US-10-081-810-54	Sequence 54, Appli
30	130	95.6	348	4	US-10-278-087A-46	Sequence 46, Appli
31	130	95.6	349	3	US-09-966-782A-11	Sequence 11, Appli
32	130	95.6	349	3	US-09-992-331-12	Sequence 12, Appli
33	130	95.6	349	3	US-09-826-509-503	Sequence 503, App
34	130	95.6	349	4	US-10-090-569-5	Sequence 5, Appli
35	130	95.6	349	4	US-10-212-980-7	Sequence 7, Appli
36	130	95.6	349	4	US-10-225-567A-126	Sequence 126, App
37	130	95.6	349	4	US-10-262-313-12	Sequence 12, Appli
38	130	95.6	349	4	US-10-166-568-2	Sequence 2, Appli
39	130	95.6	349	4	US-10-254-905-11	Sequence 11, Appli
40	130	95.6	349	4	US-10-359-285-6	Sequence 6, Appli
41	130	95.6	349	4	US-10-353-890-84	Sequence 84, Appli
42	130	95.6	349	4	US-10-768-878-12	Sequence 12, Appli
43	130	95.6	349	5	US-10-925-095-503	Sequence 503, App
44	130	95.6	349	6	US-11-060-291-17	Sequence 17, Appli
45	130	95.6	395	2	US-08-900-230-5	Sequence 5, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-362-286-1  
; Sequence 1, Application US/09362286  
; Publication No. US20020197706A1  
; GENERAL INFORMATION:  
; APPLICANT: Nadkarni, Anupama K.  
; APPLICANT: Trueheart, Joshua  
; TITLE OF INVENTION: Expression of G Protein-Coupled Receptors with Altered  
; TITLE OF INVENTION: Ligand Binding and/or Coupling Properties  
; FILE REFERENCE: CPI-099  
; CURRENT APPLICATION NUMBER: US/09/362,286  
; CURRENT FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: receptor  
; OTHER INFORMATION: sequence motif  
US-09-362-286-1

Query Match 100.0%; Score 136; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 4.2e-12; Gaps 0;  
Matches 27; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LAYNSGVSVPPIIYAFLSNFRKRYKQV 27  
|||||  
Db 1 LAYNSGVSVPPIIYAFLSNFRKRYKQV 27

##### RESULT 2

US-09-362-286-5  
; Sequence 5, Application US/09362286  
; Publication No. US20020197706A1  
; GENERAL INFORMATION:  
; APPLICANT: Nadkarni, Anupama K.  
; APPLICANT: Trueheart, Joshua  
; TITLE OF INVENTION: Expression of G Protein-Coupled Receptors with Altered  
; TITLE OF INVENTION: Ligand Binding and/or Coupling Properties  
; FILE REFERENCE: CPI-099  
; CURRENT APPLICATION NUMBER: US/09/362,286  
; CURRENT FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:43:42 ; Search time 28 Seconds  
(without alignments)  
79.723 Million cell updates/sec

Title: US-09-362-286A-1

Perfect score: 136

Sequence: 1 LAYNSNVNPIIYAFLESENFRKRYKQV 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2.6/prodata/1/iaa/5 COMB.pep.\*
- 2: /cgn2.6/prodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2.6/prodata/1/iaa/H COMB.pep.\*
- 4: /cgn2.6/prodata/1/iaa/PCTUS COMB.pep.\*
- 5: /cgn2.6/prodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2.6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	95.6	345	2	US-08-981-700A-5
2	130	95.6	346	2	US-09-199-737-5
3	130	95.6	346	2	US-08-993-088A-3
4	130	95.6	346	2	US-08-993-424B-3
5	130	95.6	346	2	US-09-058-333A-5
6	130	95.6	346	2	US-09-595-549-6
7	130	95.6	346	2	US-09-603-680-3
8	130	95.6	346	2	US-08-899-112B-30
9	130	95.6	346	2	US-09-011-553-7
10	130	95.6	348	2	US-08-513-974B-46
11	130	95.6	348	2	US-08-513-974B-342
12	130	95.6	348	2	US-08-993-088A-10
13	130	95.6	348	2	US-08-993-424B-10
14	130	95.6	348	2	US-08-540-650B-2
15	130	95.6	348	2	US-09-595-549-5
16	130	95.6	348	2	US-09-461-436B-46
17	130	95.6	348	2	US-09-603-680-10
18	130	95.6	349	2	US-08-513-974B-343
19	130	95.6	349	2	US-08-993-088A-11
20	130	95.6	349	2	US-08-993-424B-11
21	130	95.6	349	2	US-08-540-650B-5
22	130	95.6	349	2	US-08-693-308-2
23	130	95.6	349	2	US-09-595-549-7
24	130	95.6	349	2	US-09-603-680-11
25	130	95.6	349	2	US-08-981-700A-6
26	130	95.6	349	2	US-08-826-509-503
27	130	95.6	351	2	US-08-513-974B-344

Sequence 5, Appli  
Sequence 20, Appli  
Sequence 4, Appli  
Sequence 8, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 3, Appli  
Sequence 21, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 10, Appli  
Sequence 4, Appli  
Sequence 6, Appli  
Sequence 7, Appli  
Sequence 8, Appli

## ALIGNMENTS

RESULT 1  
US-08-981-700A-5  
; Sequence 5, Application US/08981700A  
; Patent No. 6562945  
; GENERAL INFORMATION:  
; APPLICANT: Walker, Philippe  
; APPLICANT: Wahlestedt, Claes  
; APPLICANT: Ahmad, Sultan  
; APPLICANT: Shen, Shi Hsiang  
; TITLE OF INVENTION: A No. 6562945el Galanin Receptor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSSEE: Vinson & Elkins L.L.P.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.  
; ZIP: 20004-1008  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,700A  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanzo, Michael A.  
; REGISTRATION NUMBER: 36,912  
; REFERENCE/DOCKET NUMBER: ABA300/67008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)639-6585  
; TELEFAX: (202)639-6604  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-981-700A-5

Query Match 95.6%; Score 130; DB 2; Length 345;  
Best Local Similarity 96.3%; Fred. No. 6.1e-11;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 LAYNSNVNPIIYAFLESENFRKRYKQV 27

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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:33:42 ; Search time 119 Seconds  
(without alignments)  
160.078 Million cell updates/sec

Title: US-09-362-286A-1  
Perfect score: 136  
Sequence: 1 LAYNSNVNPIIYAFLENFRKRYKQV 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_prot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	95.6	346	1	GALRL1 RAT
2	130	95.6	348	1	GALRL1 MOUSE
3	130	95.6	349	1	GALRL1 HUMAN
4	130	95.6	349	2	Q4VBL7 HUMAN
5	129	94.9	397	2	Q4RFJ0 TETNG
6	103	75.7	467	2	Q8MU51 DROME
7	103	75.7	483	2	Q9VVQ1 DROME
8	102	75.0	263	2	Q76873 DROME
9	102	75.0	384	2	Q917W8 DROME
10	102	75.0	394	2	Q9U721 DROME
11	101	74.3	114	2	Q7PUG9 ANOGA
12	101	74.3	144	2	Q7PY69 ANOGA
13	101	74.3	145	2	Q7PD36 ANOGA
14	100	73.5	279	2	Q7QAK0 ANOGA
15	100	73.5	380	2	Q9NFV0 LYNST
16	100	73.5	380	2	Q9NFV1 LYNST
17	100	73.5	380	2	Q9NFV2 LYNST
18	100	73.5	380	2	Q9NFV3 LYNST
19	99	72.8	361	2	Q8WPA2 BOMMO
20	99	72.8	423	2	Q964D4 PERAM
21	98.5	72.4	357	2	Q9NBC8 DROME
22	98	72.1	314	2	Q4SEW4 TETNG
23	96	70.6	370	2	Q6FQM2 HAPBU
24	96	70.6	370	2	Q8UWL5 FUGRU
25	95	69.9	372	1	OPRD HUMAN
26	95	69.9	372	1	OPRD MOUSE
27	95	69.9	372	1	OPRD RAT
28	95	69.9	372	2	Q8BLF9 MOUSE
29	95	69.9	489	2	Q8MTX9 DROME
30	95	69.9	547	2	Q81943 DROME
31	95	69.9	549	2	Q81QS9 DROME

32	94	69.1	332	2	Q7Q055 ANOGA	Q7Q055 anopheles g
33	94	69.1	371	2	Q5G84 CHICK	Q5G84 gallus gall
34	94	69.1	372	2	Q6GQ36 XENLA	Q6GQ36 xenopus lae
35	93	68.4	144	2	Q08840 RAT	Q08840 rattus norv
36	93	68.4	180	2	Q7YS17 CANFA	Q7YS17 canis faml
37	93	68.4	285	2	Q4SQUG TETNG	Q4SQUG tetraodon n
38	93	68.4	362	2	Q4RH52 TETNG	Q4RH52 tetraodon n
39	93	68.4	368	1	SSR2 BOVIN	P34993 bos taurus
40	93	68.4	369	1	SSR2 HUMAN	P30874 homo sapien
41	93	68.4	369	1	SSR2 MOUSE	P30875 mus musculu
42	93	68.4	369	1	SSR2 PIG	P34994 sus scrofa
43	93	68.4	369	1	SSR2 RAT	P30680 rattus norv
44	93	68.4	369	2	Q4VBE0 HUMAN	Q4VBP0 homo sapien
45	93	68.4	380	2	Q9DGQ6 CARAU	Q9DGQ6 carassius a

ALIGNMENTS

RESULT 1

GALRL1 RAT

ID GALRL1 RAT STANDARD; PRT; 346 AA.

AC Q62805;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 10-MAY-2005 (Rel. 47, Last annotation update)

DE Galanin receptor type 1 (GAL1-R) (GALRL1)

GN Name=Galrl; Synonyms=Galnr, Galnrl;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Insulinoma;

RX MEDLINE=96363004; PubMed=8750821; DOI=10.1016/0169-328X(95)00159-P;

RA Parker E.M., Izzarelli D.G., Nowak H.P., Mahle C.D., Iben L.G.,

RA Wang J., Goldstein M.E.;

RT "Cloning and characterization of the rat GALRL1 galanin receptor from

RL Rln4B insulinoma cells.";

RL Brain Res. Mol. Brain Res. 34:179-189(1995).

CC -!- FUNCTION: Receptor for the hormone galanin. The activity of this

CC receptor is mediated by G proteins that inhibit adenylate cyclase

CC activity.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Spinal cord, small intestine, Rln4B

CC insulinoma cells and several brain regions, particularly ventral

CC hippocampus, amygdala, supraoptic nucleus, hypothalamus, thalamus,

CC lateral parabrachial nucleus and locus coeruleus.

CC -!- PTM: Three cysteine residues are found in the C-terminus, at least

CC one of which may be palmitoylated.

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL; U30290; AAC52438.1; -; mRNA.

CC Ensembl; ENSRNOG0000016654; Rattus norvegicus.

DR RGD; 2656; Galrl.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0004966; F:galanin receptor activity; IDA.

DR GO; GO:0004293; F:neuropeptide binding; IDA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IDA.

DR InterPro; IPR000405; Galanin receptor.

DR InterPro; IPR0003906; Galnrln receptor.

DR InterPro; IPR000276; GPCR\_Rhodopsn.

DR PANTHER; PTHR19264:SF157; Galnrln\_receptor; 1.

DR Pfam; PF00001; 7cm\_1; 1.

DR PRINTS; PR01418; GALANINR1.

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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:34:02 ; Search time 18.6667 Seconds  
(without alignments)  
139.171 Million cell updates/sec

Title: US-09-362-286A-1  
Perfect score: 136  
Sequence: 1 LAYNSNVNPIIYAFLENFRKRYKQV 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	95.6	349	2 159336	galanin receptor 1
2	102	75.0	394	2 JC7209	galanin receptor -
3	99	72.8	423	2 JC7677	allatostatin recep
4	98.5	72.4	357	2 JC7319	probable allatosta
5	95	69.9	372	2 I38532	delta opioid recep
6	95	69.9	372	2 B48227	delta opioid recep
7	95	69.9	372	2 S34592	delta opioid recep
8	93	68.4	369	2 B41795	somatostatin recep
9	93	68.4	369	2 JC2083	somatostatin recep
10	93	68.4	369	2 D41795	somatostatin recep
11	93	68.4	369	2 A45291	somatostatin recep
12	91	66.9	384	2 JC4629	somatostatin recep
13	91	66.9	384	2 A47249	brain-specific som
14	91	66.9	388	2 JN0605	somatostatin recep
15	90	66.2	333	2 138974	G protein-coupled
16	90	66.2	346	2 S29248	somatostatin recep
17	90	66.2	380	2 JC2338	kappa opioid recep
18	90	66.2	380	2 A55259	kappa opioid recep
19	89	65.4	363	2 I57955	somatostatin recep
20	89	65.4	363	2 I57940	somatostatin recep
21	89	65.4	364	2 JN0763	somatostatin recep
22	89	65.4	380	2 A48227	kappa opioid recep
23	89	65.4	380	2 JC2434	kappa opioid recep
24	89	65.4	380	2 S36143	kappa opioid recep
25	86	63.2	391	2 A41795	somatostatin recep
26	86	63.2	391	2 C41795	somatostatin recep
27	86	63.2	391	2 A39297	somatostatin recep
28	86	63.2	392	2 S65693	opioid receptor mu
29	86	63.2	398	2 A57510	mu opioid receptor

30	86	63.2	398	2 156517	mu opioid receptor
31	86	63.2	398	2 156504	mu opioid receptor
32	86	63.2	400	2 156553	mu opiate receptor
33	85	62.5	373	2 JB0087	delta opioid recep
34	84	61.8	362	2 I38990	Melb-melatonin re
35	84	61.8	420	2 151666	Mel-lc receptor su
36	84	61.8	488	2 156507	histamine H1 recep
37	84	61.8	580	2 H87963	protein Y542A.1 [
38	84	61.8	643	2 T19135	cholecystokinin ty
39	83	61.0	350	2 I38848	Mel-1a melatonin r
40	82	60.3	387	2 JC5949	galanin receptor 2
41	81	59.6	289	2 S72554	melatonin receptor
42	81	59.6	340	2 JC7695	G protein-coupled
43	81	59.6	355	2 A45177	chemokine (C-C) re
44	81	59.6	358	2 JQ1278	histamine H2 recep
45	81	59.6	359	2 A39008	histamine H2 recep

ALIGNMENTS

RESULT 1

159336  
galanin receptor 1 - human  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004  
C:Accession: I59336; JC5801; G01765; G02528  
R: Habert-Ortoli, B.; Amiranoff, B.; Loquet, I.; Laburthe, M.; Mayaux, J.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9780-9783, 1994  
A:Title: Molecular cloning of a functional human galanin receptor.  
A:Reference number: I59336; MUID:95024044; PMID:7524088  
A:Accession: I59336  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-349 <HAB>  
A:Cross-references: UNIPROT:P47211; UNIPARC:UPI000004B244; GB:L34339; NID:9559047; PIDN:  
R: Lorimer, D.D.; Matkowskyj, K.; Benya, R.V.  
Biochem. Biophys. Res. Commun. 241, 558-564, 1997  
A:Title: Cloning, chromosomal location, and transcriptional regulation of the human gal;  
A:Reference number: JC5801; MUID:98086390; PMID:9425310  
A:Accession: JC5801  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-349 <LOR>  
A:Cross-references: UNIPARC:UPI000004B244; GB:U53511; NID:g1297337; PIDN:AAC51936.1; PI  
A:Note: submitted to the EMBL Data Library, April 1996  
R: Ross, P.C.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: G08350  
A:Accession: G01765  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-14 'W', 16-349 <ROS>  
A:Cross-references: UNIPARC:UPI0000050503PC; EMBL:U23854; NID:g775209; PID:g775210  
C:Comment: This receptor inhibits cAMP formation, stimulates and inhibits phospholipase  
, and increases arachadonic acid metabolism, as well as opens ATP-dependent K+ but clos  
C:Genetics:  
A:Gene: GDB:GALNR  
A:Cross-references: GDB:392699; OMIM:600377  
A:Map position: 18q23-18q23  
C:Superfamily: vertebrate rhodopsin

Query Match 95.6%; Score 130; DB 2; Length 349;  
Best Local Similarity 96.3%; Pred. No. 1e-11;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy , 1 LAYNSNVNPIIYAFLENFRKRYKQV 27  
Db 291 LAYNSNVNPIIYAFLENFRKRYKQV 317

RESULT 2

JC7209

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OM protein - protein search, using sw model

Run on: January 5, 2006, 10:56:41 ; Search time 113.333 Seconds  
(without alignments)  
104.676 Million cell updates/sec

Title: US-09-362-286A-1  
Perfect score: 136  
Sequence: 1 LAYNSVNPILYFLSENFRRYKQV 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match: 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003s:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*  
9: geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	27	6	ABU79155 Rabbit in
2	130	95.6	27	6	ABU79159 Human gal
3	130	95.6	293	7	ABM85683 Human pro
4	130	95.6	339	7	ABM85684 Mouse pro
5	130	95.6	345	8	ADR40545 Rat galan
6	130	95.6	346	2	AAI45129 Rat galan
7	130	95.6	346	4	ABM85138 Rat galan
8	130	95.6	346	5	AAQ68218 Rat galan
9	130	95.6	346	5	ABJ10558 Galanin-1
10	130	95.6	346	6	ADA09966 Rat GALR1
11	130	95.6	346	6	ABO19490 Rat galan
12	130	95.6	346	7	ADL80092 Rat galan
13	130	95.6	346	8	ADG42013 Rat galan
14	130	95.6	346	8	ADO80864 Rat galan
15	130	95.6	347	8	ADR40544 Murine ga
16	130	95.6	348	2	AAR95069 Mouse pan
17	130	95.6	348	2	ABG73523 Murine GA
18	130	95.6	348	6	ABG73523 Murine GA
19	130	95.6	348	8	ADO29348 Mouse GPC
20	130	95.6	348	9	ADZ13222 Murine ca
21	130	95.6	348	9	ADZ13220 Murine ca
22	130	95.6	349	2	AAR79443 Galanin r
23	130	95.6	349	2	AAR95070 Human gal
24	130	95.6	349	4	ABB56355 Non-endog

25	130	95.6	349	5	AAU09898	Human gal
26	130	95.6	349	5	AAU09897	Human gal
27	130	95.6	349	5	AAU09895	Human gal
28	130	95.6	349	5	AAU09899	Human gal
29	130	95.6	349	5	AAU09896	Human gal
30	130	95.6	349	6	ABP81821	Human gal
31	130	95.6	349	7	ADE31727	Human 283
32	130	95.6	349	8	ADO80863	Human gal
33	130	95.6	349	8	ADO29347	Human GPC
34	130	95.6	349	8	ADR40546	Human gal
35	130	95.6	349	9	ADZ13225	Human can
36	130	95.6	396	8	ABM84571	Human dia
37	130	95.6	690	8	ADU82874	Ligand up
38	103	75.7	451	4	ABB63156	Drosophil
39	103	75.7	451	4	AAU38949	Drosophil
40	103	75.7	451	7	ADC35829	Drosophil
41	103	75.7	451	8	ADQ87578	Antagonis
42	103	75.7	467	4	AAAB6956	D. melano
43	103	75.7	483	4	AAU03214	Fruit fly
44	103	75.7	483	7	AAE38181	Fruit fly
45	103	75.7	483	7	ADE14542	Fruit fly

ALIGNMENTS

RESULT 1  
ID ABU79155 standard; peptide; 27 AA.  
XX AC ABU79155;  
XX AC  
DT 18-JUN-2003 (first entry)  
XX XX  
DE Rabbit interleukin 8A (IL8A) receptor motif #1.  
XX XX  
KW Mutant mammalian G-protein coupled receptor; GPCR; cell transformation;  
KW cellular function modulation; interleukin 8A receptor; IL8A receptor;  
KW rabbit; motif.  
XX OS Oryctolagus cuniculus.  
XX XX  
PN US2002197706-A1.  
XX PD 26-DEC-2002.  
XX PF 27-JUL-1999; 95US-003622286.  
XX PR 28-JUL-1998; 98US-0094451P.  
XX XX (CADU-) CADUS PHARM CORP.  
XX XX Nadkarni AK, Trueheart J;  
XX XX WPI; 2003-370794/35.  
XX XX New mutant mammalian G-protein coupled receptor (GPCR) comprising a  
PT seventh transmembrane domain and at least one point mutation in the amino  
PT acid motif, useful in transforming cells for screening modulators of  
PT modified GPCR.  
XX Claim 14; Page 39; 50pp; English.  
PS The invention describes a mutant mammalian G-protein coupled receptor  
CC (GPCR) having a sequence, which varies from a wild type GPCR, comprising  
CC an amino acid motif (i) lying near the carboxy terminal end of the  
CC domain. The modified forms of GPCR are useful in transforming cells,  
CC which may be used in screening and identifying pharmaceutical compounds  
CC that specifically modulate the activity of these modified forms of GPCR.  
CC The method is useful for identifying compounds that be used for  
CC modulating cellular function, and in understanding the pharmacology of  
CC compounds that specifically interact with these modified forms of GPCR.  
CC This is the amino acid sequence of a rabbit interleukin 8A (IL8A)

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OM protein - protein search, using sw\_model

Run on: January 5, 2006, 11:56:13 ; Search time 6 Seconds  
(without alignments)  
38.191 Million cell updates/sec

Title: US-09-362-286A-3

Perfect score: 147

Sequence: 1 LGFLHSLNPIIYAFIGNFRNGFLKM 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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  - 2: /cgn2\_6/prodata1/pubpaa/US06\_NEW\_PUB.pap:\*
  - 3: /cgn2\_6/prodata1/pubpaa/US07\_NEW\_PUB.pap:\*
  - 4: /cgn2\_6/prodata1/pubpaa/PCT\_NEW\_PUB.pap:\*
  - 5: /cgn2\_6/prodata1/pubpaa/US09\_NEW\_PUB.pap:\*
  - 6: /cgn2\_6/prodata1/pubpaa/US10\_NEW\_PUB.pap:\*
  - 7: /cgn2\_6/prodata1/pubpaa/US11\_NEW\_PUB.pap:\*
  - 8: /cgn2\_6/prodata1/pubpaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	77.6	374	7	US-11-127-877-62
2	94	63.9	352	6	US-10-995-561-523
3	94	63.9	352	7	US-11-068-686-20
4	94	63.9	352	7	US-11-068-686-20
5	94	63.9	352	7	US-11-127-877-61
6	90	61.2	374	7	US-11-127-877-60
7	88	59.9	360	6	US-10-959-310-36
8	85	57.8	400	7	US-11-127-877-55
9	82	55.8	349	7	US-11-028-922A-2
10	82	55.8	432	6	US-10-992-577-2
11	81	55.1	352	7	US-11-028-922A-1
12	80	54.4	355	7	US-11-068-686-4
13	80	54.4	355	7	US-11-127-877-64
14	80	54.4	417	6	US-10-992-577-44
15	79	53.7	355	6	US-10-995-561-636
16	79	53.7	362	6	US-10-995-561-637
17	76	51.7	351	7	US-11-122-849-2
18	76	51.7	420	6	US-10-992-577-6
19	76	51.7	522	6	US-10-510-018-2
20	75	51.0	359	6	US-10-995-561-712
21	75	51.0	359	6	US-10-995-561-716
22	75	51.0	359	6	US-10-876-787-2
23	75	51.0	359	7	US-11-127-877-65
24	75	51.0	388	6	US-10-995-561-713
25	75	51.0	394	6	US-10-995-561-714

26	75	51.0	394	6	US-10-995-561-715
27	75	51.0	429	7	US-11-127-877-51
28	75	51.0	430	6	US-10-992-577-8
29	75	51.0	466	7	US-11-127-877-50
30	74	50.3	114	6	US-10-995-561-836
31	74	50.3	388	6	US-10-995-561-838
32	74	50.3	389	6	US-10-995-561-837
33	73	49.7	333	7	US-11-127-877-57
34	70	47.6	353	6	US-10-875-716-10
35	67	45.6	391	7	US-11-127-877-52
36	67	45.6	559	6	US-10-521-162-4
37	67	45.6	712	6	US-10-521-162-12
38	65	44.2	92	6	US-10-521-162-34
39	65	44.2	350	7	US-11-165-024-3
40	65	44.2	480	6	US-10-521-162-40
41	62	42.2	346	7	US-11-157-930-2
42	61	41.5	20	7	US-11-127-877-566
43	61	41.5	350	6	US-10-502-145-1
44	60	40.8	17	7	US-11-157-930-13
45	60	40.8	471	6	US-10-995-561-901

## ALIGNMENTS

RESULT 1									
US-11-127-877-62									
; Sequence 62, Application US/11127877									
; Publication NO. US20050287565A1									
; GENERAL INFORMATION:									
; APPLICANT: Merchiers, Pascal G.									
; APPLICANT: Hoffmann, Marcel									
; APPLICANT: Spittaels, Koenraad F. F.									
; APPLICANT: Laenen, Wendy									
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting									
; TITLE OF INVENTION: Amyloid-Beta Protein Production									
; FILE REFERENCE: P27, 800-B USA									
; CURRENT APPLICATION NUMBER: US/11/127, 877									
; CURRENT FILING DATE: 2005-05-12									
; PRIOR APPLICATION NUMBER: 60/570,352									
; PRIOR FILING DATE: 2004-05-12									
; PRIOR APPLICATION NUMBER: 60/603,948									
; PRIOR FILING DATE: 2004-08-24									
; NUMBER OF SEQ ID NOS: 590									
; SOFTWARE: PatentIn version 3.3									
; SEQ ID NO 62									
; LENGTH: 374									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-11-127-877-62									
Query Match 77.6%; Score 114; DB 7; Length 374;									
Best Local Similarity 74.1%; Pred. No. 1.2e-10;									
Matches 20; Conservative 3; Mismatches 4; Indels 0; Gaps 0;									
Qy	1 LGFLHSLNPIIYAFIGNFRNGFLKM 27								
Db	304 LAFLHCLNPIIYAFIGNFRNYFLKI 330								
RESULT 2									
US-10-995-561-523									
; Sequence 523, Application US/10995561									
; Publication NO. US20050272054A1									
; GENERAL INFORMATION:									
; APPLICANT: CARGILL, Michele et al.									
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH									
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF									
; TITLE OF INVENTION: DETECTION AND USES THEREOF									
; FILE REFERENCE: CL001559									
; CURRENT APPLICATION NUMBER: US/10/995,561									
; CURRENT FILING DATE: 2004-11-24									
; NUMBER OF SEQ ID NOS: 85702									

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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:55:18 ; Search time 95.3333 Seconds  
(without alignments)  
118.336 Million cell updates/sec

Title: US-09-362-286A-3

Perfect score: 147

Sequence: 1 LGFLHSLNPIIYAFIGNFRNGFLKM 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	27	US-09-362-286-3	Sequence 3, Appl
2	138	93.9	350	US-09-782-980-83	Sequence 83, Appl
3	138	93.9	350	US-09-884-430-7	Sequence 7, Appl
4	138	93.9	350	US-09-104-063-2	Sequence 2, Appl
5	138	93.9	350	US-09-893-512-9	Sequence 9, Appl
6	138	93.9	350	US-10-099-007A-15	Sequence 15, Appl
7	138	93.9	350	US-10-225-567A-463	Sequence 463, Appl
8	138	93.9	350	US-10-336-489-7	Sequence 7, Appl
9	138	93.9	350	US-10-239-423-76	Sequence 76, Appl
10	138	93.9	350	US-10-666-689-2	Sequence 2, Appl
11	138	93.9	350	US-10-436-549-546	Sequence 546, Appl
12	138	93.9	350	US-10-423-543-94	Sequence 94, Appl
13	138	93.9	350	US-10-741-601-290	Sequence 290, Appl
14	138	93.9	350	US-10-806-018-83	Sequence 83, Appl
15	138	93.9	350	US-10-712-425-546	Sequence 546, Appl
16	138	93.9	350	US-10-791-592-7	Sequence 7, Appl
17	138	93.9	350	US-10-791-166-7	Sequence 7, Appl
18	138	93.9	350	US-10-741-600-895	Sequence 835, Appl
19	138	93.9	350	US-10-773-032-546	Sequence 546, Appl
20	138	93.9	350	US-10-799-736-9	Sequence 9, Appl
21	126	85.7	369	US-10-087-192-879	Sequence 879, Appl
22	120	81.6	355	US-10-237-563-36	Sequence 36, Appl
23	118	80.3	354	US-10-411-284-11	Sequence 11, Appl
24	118	80.3	355	US-09-893-512-10	Sequence 10, Appl
25	118	80.3	355	US-10-237-563-27	Sequence 27, Appl
26	118	80.3	355	US-10-237-563-28	Sequence 28, Appl
27	118	80.3	355	US-10-237-563-29	Sequence 29, Appl

28	118	80.3	355	4	US-10-237-563-30	Sequence 30, Appl
29	118	80.3	355	4	US-10-237-563-32	Sequence 32, Appl
30	118	80.3	355	4	US-10-237-563-33	Sequence 33, Appl
31	118	80.3	355	4	US-10-237-563-34	Sequence 34, Appl
32	118	80.3	355	4	US-10-237-563-35	Sequence 35, Appl
33	118	80.3	355	5	US-10-791-592-8	Sequence 8, Appl
34	118	80.3	355	5	US-10-791-166-8	Sequence 8, Appl
35	118	80.3	355	5	US-10-799-736-10	Sequence 10, Appl
36	118	80.3	360	4	US-10-087-192-882	Sequence 882, Appl
37	118	80.3	360	4	US-10-099-007A-16	Sequence 16, Appl
38	118	80.3	360	4	US-10-225-567A-386	Sequence 386, Appl
39	118	80.3	360	4	US-10-239-423-77	Sequence 77, Appl
40	118	80.3	360	4	US-10-101-148-4	Sequence 4, Appl
41	118	80.3	360	5	US-10-690-880-25	Sequence 25, Appl
42	118	80.3	360	5	US-10-101-673-4	Sequence 4, Appl
43	118	80.3	399	4	US-10-334-143-7	Sequence 7, Appl
44	118	80.3	399	4	US-10-276-774-2394	Sequence 2394, Ap
45	118	80.3	399	5	US-10-450-763-43968	Sequence 43968, A

## ALIGNMENTS

### RESULT 1

US-09-362-286-3  
; Sequence 3, Application US/09362286  
; Publication No. US20020197706A1  
; GENERAL INFORMATION:  
; APPLICANT: Nadkarni, Anupama K.  
; TITLE OF INVENTION: Expression of G Protein-Coupled Receptors with Altered  
; TITLE OF INVENTION: Ligand Binding and/or Coupling Properties  
; FILE REFERENCE: CPI-099  
; CURRENT APPLICATION NUMBER: US/09/362,286  
; CURRENT FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: IL-8 receptor  
; OTHER INFORMATION: motif  
US-09-362-286-3

Query Match 100.0%; Score 147; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 8,7e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGFLHSLNPIIYAFIGNFRNGFLKM 27  
DB 1 LGFLHSLNPIIYAFIGNFRNGFLKM 27

### RESULT 2

US-09-782-980-83  
; Sequence 83, Application US/09782980  
; Patent No. US20020072089A1  
; GENERAL INFORMATION:  
; APPLICANT: Khodadoust, Mehran M.  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Busfield, Samantha J.  
; APPLICANT: McCarthy, Sean A.  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Gu, Wei  
; APPLICANT: White, David  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIPE, TRASH, BDSF, LRSG, AND  
; TITLE OF INVENTION: STMTS PROTEIN AND NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: MNI-121CP  
; CURRENT APPLICATION NUMBER: US/09/782,980



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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:43:42 ; Search time 28 Seconds  
(without alignments)  
79.723 Million cell updates/sec

Title: US-09-362-286a-3  
Perfect score: 147  
Sequence: 1 LGFLHSLNPIIYAFIGNFRNGFLKM 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/prodata/1/iaa/6 COMB.pap.\*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pap.\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pap.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pap.\*  
6: /cgn2\_6/prodata/1/iaa/backfilese1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	354	1	US-07-759-568-2
2	138	93.9	350	1	US-08-202-056-7
3	138	93.9	350	1	US-08-076-093A-2
4	138	93.9	350	1	US-08-450-393A-7
5	138	93.9	350	1	US-08-410-453A-1
6	138	93.9	350	1	US-08-701-265-2
7	138	93.9	350	1	US-08-410-454A-1
8	138	93.9	350	1	US-08-284-586-2
9	138	93.9	350	1	US-08-410-456A-1
10	138	93.9	350	1	US-08-805-478-2
11	138	93.9	350	1	US-08-802-627A-2
12	138	93.9	350	1	US-08-801-238-2
13	138	93.9	350	1	US-08-801-228-2
14	138	93.9	350	2	US-09-104-296-2
15	138	93.9	350	2	US-08-446-669-7
16	138	93.9	350	2	US-09-625-573-7
17	138	93.9	350	2	US-09-949-002-305
18	138	93.9	350	4	PCT-US95-00476-7
19	138	93.9	377	2	US-09-949-002-549
20	118	80.3	312	1	US-08-118-270-38
21	118	80.3	312	4	PCT-US93-08528-38
22	118	80.3	355	1	US-07-759-568-1
23	118	80.3	355	1	US-08-450-393A-8
24	118	80.3	355	1	US-08-390-000A-5
25	118	80.3	355	2	US-08-446-669-8
26	118	80.3	355	2	US-09-625-573-8
27	118	80.3	355	4	PCT-US95-00476-8

28	118	80.3	360	1	US-08-202-056-7	Sequence 7, Appli
29	118	80.3	360	2	US-09-409-778-4	Sequence 4, Appli
30	114	77.6	365	2	US-09-503-219B-8	Sequence 8, Appli
31	114	77.6	365	2	US-10-039-659A-10	Sequence 10, Appli
32	114	77.6	374	2	US-09-045-583-48	Sequence 48, Appli
33	114	77.6	374	2	US-09-534-185-48	Sequence 48, Appli
34	114	77.6	374	2	US-09-721-341-8	Sequence 8, Appli
35	114	77.6	374	2	US-09-721-495B-8	Sequence 8, Appli
36	94	63.9	352	2	US-08-466-343D-2	Sequence 13, Appli
37	94	63.9	352	2	US-09-087-232A-13	Sequence 13, Appli
38	94	63.9	352	2	US-08-861-105-14	Sequence 14, Appli
39	94	63.9	352	2	US-08-575-967A-2	Sequence 2, Appli
40	94	63.9	352	2	US-09-045-583-52	Sequence 52, Appli
41	94	63.9	352	2	US-09-517-605-5	Sequence 52, Appli
42	94	63.9	352	2	US-09-534-185-52	Sequence 52, Appli
43	94	63.9	352	2	US-08-833-753-5	Sequence 2, Appli
44	94	63.9	352	2	US-09-502-783A-2	Sequence 2, Appli
45	94	63.9	352	2	US-09-796-202-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-07-759-568-2  
; Sequence 2, Application US/07759568  
; Patent No. 5374506  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Philip M.  
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional  
; TITLE OF INVENTION: Human Interleukin-8 Receptor  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cushman, Darby & Cushman  
; STREET: 1615 L Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/759,568  
; FILING DATE: 19910913  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scott, Watson T.  
; REGISTRATION NUMBER: 26581  
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 cush  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 354 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-759-568-2

Query Match 100.0%; Score 147; DB 1; Length 354;  
Best Local Similarity 100.0%; Pred. No: 2.2e-12;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LGFLHSLNPIIYAFIGNFRNGFLKM 27  
DB 297 LGFLHSLNPIIYAFIGNFRNGFLKM 323

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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:33:42 ; Search time 119 Seconds  
(without alignments)  
160.078 Million cell updates/sec

Title: US-09-362-286A-3  
Perfect score: 147  
Sequence: 1 LGFLHSLCINPIIYAFICQNFNGFLKM 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	147	100.0	355	1	CXCR1_RABIT
2	138	93.9	350	1	CXCR1_GORGO
3	138	93.9	350	1	CXCR1_HUMAN
4	138	93.9	350	1	CXCR1_PANTR
5	138	93.9	350	2	Q53R18_HUMAN
6	138	93.9	350	2	Q8N6T6_HUMAN
7	138	93.9	350	2	Q6IN95_HUMAN
8	126	85.7	359	1	CXCR2_MOUSE
9	126	85.7	359	1	CXCR2_RAT
10	126	85.7	359	2	Q53X27_MOUSE
11	123	83.7	351	2	Q810W6_MOUSE
12	123	83.7	352	2	Q810T4_CAVPO
13	123	83.7	358	1	CXCR2_RABIT
14	120	81.6	355	2	Q8HZN4_CERP
15	120	81.6	356	1	CXCR2_CANFA
16	120	81.6	360	1	CXCR2_BOVIN
17	118	80.3	353	1	CXCR2_MACMU
18	118	80.3	353	1	CXCR2_PANTR
19	118	80.3	355	2	Q8HZN5_MACMU
20	118	80.3	355	2	Q8HZN6_PONPY
21	118	80.3	355	2	Q8HZN7_9PRIM
22	118	80.3	355	2	Q8HZN8_PANTR
23	118	80.3	360	1	CXCR2_HUMAN
24	118	80.3	360	2	Q53PC4_HUMAN
25	117	79.6	349	1	CXCR1_RAT
26	117	79.6	367	2	Q9R1V0_MOUSE
27	114	77.6	174	2	Q9TU48_BOVIN
28	114	77.6	174	2	Q9TQ57_BOVIN
29	114	77.6	355	2	Q8HZN3_PAPHA
30	114	77.6	374	1	CCR6_HUMAN
31	114	77.6	374	2	Q53E25_HUMAN

32	114	77.6	374	2	Q8HZR7_MACMU
33	112	76.2	367	1	CCR6_MOUSE
34	112	76.2	367	2	Q542B6_MOUSE
35	110	74.8	353	1	CXCR2_GORGO
36	107	72.8	366	2	Q5BK58_RAT
37	104	70.7	353	2	Q8QF5_XENLA
38	104	70.7	392	2	Q93281_CHICK
39	102	69.4	372	2	Q93237_CIPCA
40	96	65.3	352	2	Q5MD63_BOVIN
41	95	64.6	235	2	Q4T2C0_TESTING
42	95	64.6	318	2	Q4SMC3_TESTING
43	94.5	64.3	352	2	Q6WN97_CBBPV
44	94.5	64.3	352	2	Q6WN98_CALHU
45	94	63.9	297	2	Q4RRCT_TESTING

Q8hzt7	macaca mula
Q54689	mus musculus
Q542b6	mus musculus
Q28422	gorilla gor
Q5bk58	rattus norv
Q8qfr5	xenopus lae
Q93281	gallus gall
Q93237	cyprinus ca
Q5md63	boe taurus
Q4t2c0	tetraodon n
Q4smc3	tetraodon n
Q6wn97	cabuella py
Q6wn98	callithrix
Q4rrct	tetraodon n

#### ALIGNMENTS

#### RESULT 1

ID	CXCR1_RABIT	STANDARD;	PRT;	395 AA.
AC	P21109;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	High affinity interleukin-8 receptor A (IL-8R A) (CXCR-1).			
GN	Name=IL8RA; Synonyms=CXCR1;			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;			
OC	Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=91378994; PubMed=1898400;			
RA	Beckmann M.F., Munger W.E., Kozlosky C., Vanden Bos T., Price V.,			
RA	Lyman S., Gerard N.P., Gerard C., Cerretti D.P.;			
RT	"Molecular characterization of the interleukin-8 receptor.";			
RL	J. Biol. Chem. 265:20061-20064(1990).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Neutrophil;			
RC	MEDLINE=92148149; PubMed=1737938;			
RX	Lee J., Kuang W.-J., Rice G.C., Wood W.I.;			
RA	"Characterization of complementary DNA clones encoding the rabbit IL-8			
RT	receptor.";			
RL	J. Immunol. 148:1261-1264(1992).			
CC	-I- FUNCTION: Receptor to interleukin-8, which is a powerful			
CC	neutrophils chemotactic factor. Binding of IL-8 to the receptor			
CC	causes activation of neutrophils. This response is mediated via a			
CC	G-protein that activate a phosphatidylinositol-calcium second			
CC	messenger system.			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- TISSUE SPECIFICITY: Neutrophils.			
CC	-I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.			
CC	-I- CAUTION: Was originally (Ref.2) thought to be the receptor for			
CC	fMet-Leu-Phe (N-formyl peptide receptor).			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	-----			
DR	EMBL; M74240; AAA31375.1; -; Genomic DNA.			

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OM protein - protein search, using sw model

Run on: January 5, 2006, 11:34:02 ; Search time 18.6667 Seconds  
(without alignments)  
139.171 Million cell updates/sec

Title: US-09-362-286A-3  
Perfect score: 147  
Sequence: 1 LGFLHSLNPIIYAFIGNFRNGFLKM 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	354	2 A23669	interleukin-8 rece
2	147	100.0	355	2 JQ1231	interleukin-8 rece
3	138	93.9	350	2 A39445	interleukin-8 rece
4	126	85.7	356	2 A42096	interleukin-8 rece
5	126	85.7	359	2 A48921	interleukin-8 rece
6	123	83.7	358	2 A53752	interleukin-8 rece
7	118	80.3	360	2 A53611	interleukin-8 rece
8	114	77.6	369	2 JC5068	G protein-coupled
9	94	63.9	352	2 A31113	chemokine (C-C) re
10	90	61.2	360	2 JC4587	chemokine (C-C) re
11	90	61.2	374	2 I38450	chemokine (C-C) re
12	89	60.5	367	2 JC2421	opioid receptor ho
13	89	60.5	367	2 I49022	kappa opioid recep
14	89	60.5	367	2 I56520	G protein-coupled
15	89	60.5	370	2 S43087	orphan opioid rece
16	89	60.5	444	2 T27866	hypothetical prote
17	88	59.9	360	2 A57160	chemokine (C-C) re
18	88	59.9	763	2 T24367	hypothetical prote
19	87	59.2	352	2 G00048	fusin (LESTRA) - c
20	87	59.2	360	2 JC2443	chemokine (C-C) re
21	86	58.5	362	2 JN0694	angiotensin II rec
22	86	58.5	580	2 H07963	protein Y54E2A.1 l
23	86	58.5	643	2 T19135	cholecystokinin ty
24	85	57.8	367	2 JE0349	interferon-inducib
25	85	57.8	392	2 S65693	opioid receptor mu
26	85	57.8	398	2 A57510	mu opioid receptor
27	85	57.8	398	2 I56517	mu opioid receptor
28	85	57.8	398	2 I56504	mu opioid receptor
29	85	57.8	400	2 I56553	mu opiate receptor

30 84 57.1 350 2 JN0621 G protein-coupled  
31 84 57.1 357 2 JC7319 probable allatosta  
32 84 57.1 394 2 JC7209 galanin receptor -  
33 84 57.1 423 2 JC7677 allatostatin recep  
34 83 56.5 351 2 B42009 FMPL-related recep  
35 83 56.5 353 2 C42009 FMPL-related recep  
36 81 55.1 323 1 Q0BED3 HHRF3 protein - hu  
37 81 55.1 350 2 A42009 N-formyl peptide r  
38 81 55.1 352 2 A45747 neuropeptide Y/pep  
39 81 55.1 353 2 S28787 neuropeptide Y/pep  
40 81 55.1 364 2 A49542 N-formyl peptide c  
41 80 54.4 355 2 G02436 chemokine (C-C) re  
42 80 54.4 355 2 JC5067 G protein-coupled  
43 80 54.4 355 2 A45177 chemokine (C-C) re  
44 80 54.4 359 2 I49341 MIP-1 alpha recept  
45 80 54.4 383 2 S55594 G protein-coupled

## ALIGNMENTS

### RESULT 1

A23669  
interleukin-8 receptor, high affinity - rabbit  
N/Alternate names: FMPL receptor  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C/Accession: A23669  
R/Thomas, K.M.; Pyun, H.Y.; Navarro, J.  
J. Biol. Chem. 265, 20061-20064, 1990  
A/Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.  
A/Reference number: A23669; MUID:91056034; PMID:1700779  
A/Accession: A23669  
A/Molecule type: mRNA  
A/Residues: 1-354 <THO>  
A/Cross-references: UNIPROT:P21109; UNIPARC:UPI0000156PB7; GB:M58021; GB:J05705; NID:9161  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 100.0%; Score 147; DB 2; Length 354;  
Best Local Similarity 100.0%; Pred. No: 1.9e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LGFLHSLNPIIYAFIGNFRNGFLKM 27  
|||||  
Db 297 LGFLHSLNPIIYAFIGNFRNGFLKM 343  
|||||

### RESULT 2

JQ1231  
interleukin-8 receptor - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: JQ1231; A46483  
R/Beckmann, M.P.; Munger, W.B.; Kozlosky, C.; Vandenberg, T.; Price, V.; Lyman, S.; Garavito  
Biochem. Biophys. Res. Commun. 179, 784-789, 1991  
A/Title: Molecular characterization of the interleukin-8 receptor.  
A/Reference number: JQ1231; MUID:91378994; PMID:1898400  
A/Accession: JQ1231  
A/Molecule type: DNA  
A/Residues: 1-355 <BEC>  
A/Cross-references: UNIPROT:P21109; UNIPARC:UPI000012D4ED; GB:M74240; NID:9165438; PIDN:1  
R/Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.  
J. Immunol. 148, 1261-1264, 1992

A/Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.  
A/Reference number: A46483; MUID:92148149; PMID:1737938

A/Status: preliminary  
A/Accession: A46483  
A/Molecule type: mRNA

A/Residues: 1-355 <LEB>  
A/Cross-references: UNIPARC:UPI000012D4ED; GB:M82873; NID:9165440; PIDN:AAA31376.1; PID:9  
A/Experimental source: neutrophils  
A/Note: sequence extracted from NCBI backbone (NCBI:81526, NCBI:81530)

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# OM protein - protein search, using sw model

Run on: January 5, 2006, 10:56:41 ; Search time 113.333 Seconds  
(without alignments)  
104.676 Million cell updates/sec

Title: US-09-362-286a-3

Perfect score: 147  
Sequence: 1 LGFLHSLNPIIYAFQGNFRNGFLQM 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	27	6	ABU79157
2	147	100.0	354	2	AAR53932
3	147	100.0	355	2	AAR28272
4	147	100.0	355	2	AAR80950
5	147	100.0	355	6	ABU79168
6	138	93.9	350	2	AAR27791
7	138	93.9	350	2	AAR80951
8	138	93.9	350	2	AAR68811
9	138	93.9	350	2	AAR80756
10	138	93.9	350	2	AAB09989
11	138	93.9	350	4	AAG80120
12	138	93.9	350	5	AAR17035
13	138	93.9	350	5	AAG80700
14	138	93.9	350	5	ABP54801
15	138	93.9	350	6	ABP81988
16	138	93.9	350	8	ADM10222
17	138	93.9	350	8	ADL14211
18	138	93.9	350	8	ADO29522
19	138	93.9	350	8	ADQ39172
20	138	93.9	350	8	ADR71388
21	138	93.9	350	8	ADR45611
22	138	93.9	350	8	ADS34872
23	138	93.9	350	9	ADY95725
24	138	93.9	350	9	ADZ36302

25	138	93.9	350	9	AEB22125
26	138	93.9	1060	2	AAR70123
27	126	85.7	359	7	ADA48095
28	126	85.7	359	8	ADO29525
29	126	85.7	369	7	ABM85488
30	123	83.7	351	8	ADO29523
31	123	83.7	358	2	AAR28274
32	123	83.7	358	2	AAR80952
33	120	81.6	355	5	AAU80491
34	118	80.3	312	2	AAR48717
35	118	80.3	312	2	AAW02689
36	118	80.3	354	8	ADH61817
37	118	80.3	355	2	AAR33420
38	118	80.3	355	2	AAB09990
39	118	80.3	355	5	AAU80483
40	118	80.3	355	5	AAU80489
41	118	80.3	355	5	AAU80485
42	118	80.3	355	5	AAU80488
43	118	80.3	355	5	AAU80482
44	118	80.3	355	5	AAU80487
45	118	80.3	355	5	AAU80484

## ALIGNMENTS

RESULT 1  
ABU79157

ID ABU79157 standard; peptide; 27 AA.

AC ABU79157;

DT 18-JUN-2003 (first entry)

DE Rabbit interleukin 8A (IL8A) receptor motif #3.

KW Mutant mammalian G-protein coupled receptor; GPCR; cell transformation;  
KW cellular function modulation; interleukin 8A receptor; IL8A receptor;  
KW rabbit; motif.

OS Oryctolagus cuniculus.

PN US2002197706-A1.

PD 26-DEC-2002.

PF 27-JUL-1999; 99US-00362286.

PR 28-JUL-1998; 98US-0094451P.

PA (CADU-) CADUS PHARM CORP.

PI Nadkarni AK, Trueheart J;

DR WPI; 2003-370794/35.

PT New mutant mammalian G-protein coupled receptor (GPCR) comprising a  
seventh transmembrane domain and at least one point mutation in the amino  
acid motif, useful in transforming cells for screening modulators of  
modified GPCR.

PS Example 3; Page 30; 50pp; English.

XX The invention describes a mutant mammalian G-protein coupled receptor  
(GPCR) having a sequence, which varies from a wild type GPCR, comprising  
an amino acid motif (I) lying near the carboxy terminal end of the  
domain. The modified forms of GPCR are useful in transforming cells,  
which may be used in screening and identifying pharmaceutical compounds  
that specifically modulate the activity of these modified forms of GPCR.  
The method is useful for identifying compounds that be used for  
modulating cellular function, and in understanding the pharmacology of  
compounds that specifically interact with these modified forms of GPCR.  
This is the amino acid sequence of a rabbit interleukin 8A (IL8A)